(1) GENERAL INFORMATION:
  (i) APPLICANTS:Knuth, Alexader; Jager, Elke; Chen, Yao,
          Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

  (ii) TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
      AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
      MHC CLASS I AND MHC CLASS II MOLECULES, AND **RECEIVED**
      USES THEREOF

  (iii) NUMBER OF SEQUENCES: 15   JUN 1 8 2003

  (iv) CORRESPONDENCE ADDRESS: **TECH CENTER 1600/2900**
      (A) ADDRESSEE: FULBRIGHT & JAWORSKI LLP
      (B) STREET: 666 Fifth Avenue
      (C) CITY: New York City
      (D) STATE: New York
      (E) COUNTRY:USA
      (F) ZIP: 10158

  (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
      (B) COMPUTER: IBM
      (C) OPERATING SYSTEM: PC-DOS
      (D) SOFTWARE: WordPerfect

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: 09/062,422
      (B) FILING DATE: October 2, 1998
      (C) CLASSIFICATION: 530

  (vii) PRIOR APPLICATION DATA:
      (A)APPLICATION NUMBER: 08/937,263
      (B)FILING DATE: April 17, 1998

  (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/937,263
      (B) FILING DATE: September 15, 1997

  (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: US 08/752,182
      (B) FILING DATE: 03-October-1996

  (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Hanson, Norman D.
      (B) REGISTRATION NUMBER: 30,946
      (C) REFERENCE/DOCKET NUMBER: LUD 5466.3

  (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (212) 688-9200
      (B) TELEFAX: (212) 838-3884

(2)   INFORMATION FOR SEQ ID NO: 1:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 752 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
ATCCTCGTGG GCCCTGACCT TCTCTCTGAG AGCCGGGCAG AGGCTCCGGA GCC          53
ATG CAG GCC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT          98

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala
                5                  10                 15
GAT GGC CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT         143

Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn
                20                 25                 30
GCT GGC GGC CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC         188

Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Aly Pro
                35                 40                 45
CGG GGC GCA GGG GCA GCA AGG GCC TCG GGG CCG GGA GGA GGC GCC         233

Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala
                50                 55                 60
CCG CGG GGT CCG CAT GGC GGC GCG GCT TCA GGG CTG AAT GGA TGC         278
Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys
                65                 70                 75
TGC AGA TGC GGG GCC AGG GGG CCG GAG AGC CGC CTG CTT GAG TTC         323
Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe
                80                 80                 90
TAC CTC GCC ATG CCT TTC GCG ACA CCC ATG GAA GCA GAG CTG GCC         368
Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala
                95                100                105
CGC AGG AGC CTG GCC CAG GAT GCC CCA CCG CTT CCC GTG CCA GGG         413
Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly
                110                115                120
GTG CTT CTG AAG GAG TTC ACT GTG TCC GGC AAC ATA CTG ACT ATC         458
Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile
                125                130                135
CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG CAG CTC TCC ATC AGC         503
Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser
                140                145                150
TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG ATC ACG CAG TGC         548
```

```
Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys
              155                160                165


TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG CAG AGG CGC        593
Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg
              170                175                180


TAA GCCCAGCCTG GCGCCCCTTC CTAGGTCATG CCTCCTCCCC TAGGGAATGG        646
TCCCAGCACG AGTGGCCAGT TCATTGTGGG GGCCTGATTG TTTGTCGCTG GAGGAGGACG  706
GCTTACATGT TTGTTTCTGT AGAAAATAAA ACTGAGCTAC GAAAAA               752
```

(2)   INFORMATION FOR SEQ ID NO: 2:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 31 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
CACACAGGAT CCATGGATGC TGCAGATGCG G                                31
```


(2)   INFORMATION FOR SEQ ID NO: 3:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 32 base pairs
              (B) TYPE: nuclear acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
CACACAAAGC TTGGCTTAGC GCCTCTGCCC TG                               32
```


(2)   INFORMATION FOR SEQ ID NO: 4:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 11 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Ser Leu Leu Met Trp Ile Thr Gln Cys Phe Leu
              5                10
```


(2)   INFORMATION FOR SEQ ID NO: 5:
        (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ser Leu Leu Met Trp Ile Thr Gln Cys
                    5

(2)   INFORMATION FOR SEQ ID NO: 6:
          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 9 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Leu Ser Leu Leu Met Trp Ile Thr
                    5

(2)   INFORMATION FOR SEQ ID NO: 7:
          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 10 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Leu Met Trp Ile Thr Gln Cys Phe Leu
                    5   10

(2)   INFORMATION FOR SEQ ID NO: 8:
          (i) SEQUENCE CHARACTERISTICS
                    (A) LENGTH: 18 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln
                    5   10   15

Gln Leu

(2)   INFORMATION FOR SEQ ID NO: 9:
          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 18 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile Arg
           5   10   15

Leu Thr

(2)   INFORMATION FOR SEQ ID NO: 10:
       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser Gly
           5   10   15

Asn Ile

(2)   INFORMATION FOR SEQ ID NO: 11:
       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg Gly
           5   10   15

Pro Glu

(2)   INFORMATION FOR SEQ ID NO: 12:
       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala Thr Pro Met
           5   10   15

Glu Ala

(2)   INFORMATION FOR SEQ ID NO: 13:
       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Thr Val Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His

```
                    5                    10                   15
```

Arg Gln

(2)   INFORMATION FOR SEQ ID NO: 14:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 6 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Leu Met Trp Ile Thr
                  5

(2)   INFORMATION FOR SEQ ID NO: 15:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 180 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala

                  5   10   15

Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn

                  20   25   30

Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Aly Pro

                  35   40   45

Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala

                  50   55   60

Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys

                  65   70   75

Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe

                  80   85   90

Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala

                  95   100   105

Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly
                    110   115   120

Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile
                    125   130   135

Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser
                    140   145   150

Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys
                    155   160   165

Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg
                    170   175   180